RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/735,600

Source: OIPE

Date Processed by STIC: 12-30-03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/735,600

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
        Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                          prevent "wrapping."

2_____Invalid Line Length   The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3_____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
        Numbering   use **space characters**, instead.

4_____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
                   ensure your subsequent submission is saved in ASCII text.**

5_____Variable Length   Sequence(s)_____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
                         each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
                         residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
        "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                      previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                      the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
                      Artificial or Unknown sequences.**

7_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
        (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                           (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                           (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                           This sequence is intentionally skipped

                           Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8_____Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
        (NEW RULES)   <210> sequence id number
                           <400> sequence id number
                           000

9_____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
        (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                             In <220> to <223> section, please explain location of n or Xaa, and which residue n or **Xaa** represents.

10_X_Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
        Response   -   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
                        is Artificial Sequence

11_____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
                       Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                       "Unknown." Please explain source of genetic material in <220> to <223> section.
                       (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
        "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                      listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n/Xaa   "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

RAW SEQUENCE LISTING   DATE: 12/30/2003
PATENT APPLICATION: **US/10/735,600**   TIME: 16:02:58

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\12302003\J735600.raw**

```
   4 <110> APPLICANT: Genesis Group Inc.
   5       Xie, Ya-Gang
   7 <120> TITLE OF INVENTION: Method for the Detection of Risk Factors
   8       Associated with Myocardial Infarction
  11 <130> FILE REFERENCE: 2288-0103P
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/735,600
C--> 14 <141> CURRENT FILING DATE: 2003-12-12
  16 <150> PRIOR APPLICATION NUMBER: 2,414,301
  17 <151> PRIOR FILING DATE: 2002-12-13
  19 <160> NUMBER OF SEQ ID NOS: 9
  21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
  23 <210> SEQ ID NO: 1
  24 <211> LENGTH: 1086
  25 <212> TYPE: DNA
  26 <213> ORGANISM: Homo Sapiens
  28 <400> SEQUENCE: 1
  29 ctcaccagct gtgtctcgtg aaggggcgtg gctgggctat gagctatgct cctgagcaca 60
  30 gacggctgtt ctctttcaag gttacaagcc tgatgaaggg aaacgagggg atgcctgtga 120
  31 aggtgacagt gggggaccct ttgtcatgaa ggtaagcttc tctaaagccc agggcctggt 180
  32 gaacacatct tctggggggtg gggagaaact ctagtatcta gaaacagttg cctggcaggg 240
  33 gaatactgat gtgaccttga acttgactct attggaaacc tcatctttct tcttcagagc 300
  34 cccttaaca accgctggta tcaaatgggc atcgtctcat ggggtgaagg ctgtgaccgg 360
  35 gatgggaaat atggcttcta cacacatgtg ttccgcctga agaagtggat acagaaggtc 420
  36 attgatcagt ttggagagta gggggccact catattctgg gctcctggaa ccaatcccgt 480
  37 gaaagaatta tttttgtgtt tctaaaacta tggttcccaa taaaagtgac tctcagcaag 540
  38 cctcaatgct cccagtgcta ttcatgggca gctctctggg ctaggaagag ccagtaatac 600
  39 tactggataa agaagactta agaatccacc acctggtgca cgctggtagt ccgagcactc 660
  40 gggaggctga ggtgggagga tcgcttgagc ccaggaggtg gaggctgcag tgagccactg 720
  41 cacccccagcc tgggtgacag agtgagaccc tgtcccaaaa gaatccacta tctatcttca 780
  42 gagcagggcc aggtgagagg aaagatggca ggttgaattt acaggcatta aagatgttcc 840
  43 accctctggg ttttaatgga ttatctcatt taatcctcac aagaggtagg tgagtaaact 900
  44 gagatttgga gaagtacctt gtccaaagtc acatggctaa gaaagctcaa agtaggactt 960
  45 caaatataga aaatattgag tgaggacggt gctttttag ttaactccct acatcttccc 1020
  46 ttgtatcatt aaaatgatat cagatcaggt agggcatggt ggctcacacc tgtaatctca 1080
  47 gcaatt                                                        1086
  49 <210> SEQ ID NO: 2
  50 <211> LENGTH: 20
  51 <212> TYPE: DNA
  52 <213> ORGANISM: Primer
  54 <400> SEQUENCE: 2
  55 tctagaaaca gttgcctggc                                           20
  57 <210> SEQ ID NO: 3
  58 <211> LENGTH: 22
```

Does Not Comply Corrected Diskette Needed (handwritten stamp)

See item 10 on error summary report. (handwritten)

```
 59 <212> TYPE: DNA
 60 <213> ORGANISM: Primer
 62 <400> SEQUENCE: 3
 63 atagcactgg gagcattgaa gc                                    22
 65 <210> SEQ ID NO: 4
 66 <211> LENGTH: 480
 67 <212> TYPE: DNA
 68 <213> ORGANISM: Homo Sapiens
 70 <400> SEQUENCE: 4
 71 gcaaatgaaa acaattttga atatattttc tttcaggcag gaacaacacc atgatcagag 60
 72 cagttcaacc aggggaaacc tatacttata agtggaacat cttagagttt gatgaaccca 120
 73 cagaaaatga tgcccagtgc ttaacaagac catactacag tgacgtggac atcatgagag 180
 74 acatcgcctc tgggctaata ggactacttc taatctgtaa gagcagatcc ctggacaggc 240
 75 aaggaataca ggtattttgt ccttgaagta acctttcaga aattctgaga atttcttctg 300
 76 gctagaacat gttaggtctc ctggctaaat aatggggcat ttccttcaag agaacagtaa 360
 77 ttgtcaagta gtccttttta gcaccagtgt gataacattt attctttttt tttttttgtc 420
 78 ttgtctattt ttatcagtac catcactgcc gaaggcaagt ctagagtgtg ataacatatt 480
 81 <210> SEQ ID NO: 5
 82 <211> LENGTH: 21
 83 <212> TYPE: DNA
 84 <213> ORGANISM: Primer
 86 <400> SEQUENCE: 5
 87 acccacagaa aatgatgccc a                                     21
 89 <210> SEQ ID NO: 6
 90 <211> LENGTH: 21
 91 <212> TYPE: DNA
 92 <213> ORGANISM: Primer
 94 <400> SEQUENCE: 6
 95 tgccccatta tttagccagg a                                     21
 97 <210> SEQ ID NO: 7
 98 <211> LENGTH: 653
 99 <212> TYPE: DNA
100 <213> ORGANISM: Homo Sapiens
102 <400> SEQUENCE: 7
103 ttccatatgt tttgacacat acaaaaatct ccccaagatc cttggggaac tgtattccat 60
104 cattagacta atccttgctg ccacttctca gttttttattt atgcaaacgg caaaatgtgt 120
105 tgctcaagtg ctatcacaca cagatatatc tgtttctcta ttttggaatc cttgtctcaa 180
106 atgttactca ctttacatgc cttttctgtt gtcttctttt tttttttttt ctgaaggacc 240
107 ttgtaaagtc aaaaatgtca gaaacttcca ggaccgcctt tggaggcaga agagcagttc 300
108 cacccaataa ctctaatgca gcggaagatg acctgcccac agtggagctt cagggcttgg 360
109 tgccccgggg cgtcaacctg caaggtatga gcataccccc cttccccacc actctgggtc 420
110 caggcacagc cgggccctgg cccctcttcc ctgcaggtaa acatcctctg tctccactgg 480
111 ggttcccaca aaaggaagcc ccctgccaat ctctggtttt ataaaggaag aaagcaaaag 540
112 ctttctttta agtggtgaaa gcaccgaaga cccagagcct tgtcccagtt ctgcccctta 600
113 ctgaccttgt aacctcagag aagttgcttt gtctttctgc ctctcaacta ttt        653
115 <210> SEQ ID NO: 8
116 <211> LENGTH: 21
117 <212> TYPE: DNA
118 <213> ORGANISM: Primer
```

Same error

RAW SEQUENCE LISTING DATE: 12/30/2003
PATENT APPLICATION: **US/10/735,600** TIME: 16:02:58

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\12302003\J735600.raw**

```
120 <400> SEQUENCE: 8
121 catgcctttt ctgttgtctt c                                        21
123 <210> SEQ ID NO: 9
124 <211> LENGTH: 30
125 <212> TYPE: DNA
126 <213> ORGANISM: Primer        Same error
128 <400> SEQUENCE: 9
129 taccttgcag gttgacgccc cggggcacta                               30
```

VERIFICATION SUMMARY   DATE: 12/30/2003
PATENT APPLICATION: **US/10/735,600**   TIME: 16:02:59

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\12302003\J735600.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date